

Figure 3 continued

131 GGYELWIKAFLLLVGFWSLLYMMCTLDPSFGAILAAMSLGVFAAFVGTCT 180
228 QHDSNMGAFSRNTLVNRLAGWMDLIGASSTVWEYQHVIGHHQYTNLVS: 276
|||||... ||:|||| ||:|||| ||:|||| ||:||||
181 QHDSNMGAFASRWVNVKVGWTLDMIGASGMTWEFQHVLGHHPTYTNLIEE 230
277DTLFLSPENDPDVFSSYPLMRMHPDTAWQPHHRFQHLF 314
|| . |||||.||:|||| . :||||:
231 ENGLQKVSCKMDTKIADQESDPDVFSTYPMRLHPWHQKRWYHRFQHIY 280
315 APPLFALMTISKVLTSDFAVCLSMKKGSIDCSSRLVPLEGQLLFWGAKLA 364
:| |||.||. | | : | | | | | | | |
281 GPFIFGFMNTINKVVTQDVGVLRLKRLFQIDAECRYASPMYVARFWIMKAL 330
365 NFLLIQIVLPCYLHGTAMGLALFSVAHLVSGEYLAICFIINHISESCEFMN 414
| : ||||: | || ||:|||| || || ||:|||| | :
331 TVLYMVVALPCYMQGPWHGLKLFALIAHFTCGEVLATMFIVNHIIEGVSYAS 380
415 TSF.....QTAARRTEMLQAAHQ.AEAKK...VKPTPPNDWAVTQ 452
. | | | : ||| | | . | | | |
381 KDAVKGTMAPPKTMHGVTPMNTRKEVEAEASKGAVVKSVPPLDDWAVVQ 430
453 VQCCVNRSGGVLANHLGGGLNHQIEHHLFPSISHANYPTIAPVVKVECE 502
| ||| | || ||||| ||||| : || | | | |
431 CQTSVNVSVGSWFNHFSGGLNHQIEHHLFPGLSHETYYHIQDVFQSTCA 480

Figure 3 continued

503 EYGLPYKNYVTFWDVCGMVQHRLRLMGAPPVPTNGDKKS* 542

|||.||.. . | | |. : || | : |

481 EYGVYPYQHEPSLWTAYWKMLEHLRQLGNEETHESWQRAA* 520